STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/926,493_
Source: _IFwP_
Date Processed by STIC: _3/14/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
                     prevent "wrapping."

2 ____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
      Numbering   use **space characters**, instead.

4 ____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5 ____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7 ____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
      (NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 ____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence. (see item 11 below)

11 ____Use of <220>   Sequence(s)____missing the <220> "Feature" and associated numeric identifiers and responses. Use
of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
Sequence Rules

12 ____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____Misuse of n/Xaa   "n" can **only** represent a single nucleotide; "Xaa" can only represent a single amino acid

IFWP

```
RAW SEQUENCE LISTING              DATE: 03/14/2006
PATENT APPLICATION:  US/09/926,493   TIME: 10:53:43

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\03142006\I926493.raw
```

see item 2 on Err Summary Sheet

```
     3 <110> APPLICANT: Centre National De La Recherche Scientifique (CNRS)
     5 <120> TITLE OF INVENTION: Nucleic Acid-Antibody Conjugate for Delivering A Foreign
Nucleic Acid
     6       into Cells
     8 <130> FILE REFERENCE: P67289US0
    10 <140> CURRENT APPLICATION NUMBER: US 09/926,493
C--> 12 <141> CURRENT FILING DATE: 2001-11-13
    14 <150> PRIOR APPLICATION NUMBER: FR 99/05943
    16 <151> PRIOR FILING DATE: 1999-05-10
E--> 18 <160> NUMBER OF SEQ ID NOS: 2    5 (p.4)
    20 <170> SOFTWARE: PatentIn version 3.1
```

pp 1, 3-4

ERRORED SEQUENCES

9 shown below

```
    22 <210> SEQ ID NO: 1
    24 <211> LENGTH: 8
    26 <212> TYPE: PRT
    28 <213> ORGANISM: Artificial Sequence
    30 <220> FEATURE:
    32 <221> NAME/KEY: MISC_FEATURE
    34 <222> LOCATION: (1)...(2)
    36 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of the
antibody
    38 <400> SEQUENCE: 1
W--> 40 Xaa Xaa Phe Tyr Gly Gly Phe Arg Leu
E--> 41 1              5
    44 <210> SEQ ID NO: 2
    46 <211> LENGTH: 8
    48 <212> TYPE: PRT
    50 <213> ORGANISM: Artificial Sequence
    52 <220> FEATURE:
    54 <221> NAME/KEY: MISC_FEATURE
    56 <222> LOCATION: (1)...(2)
    58 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of the
antibody
    60 <400> SEQUENCE: 2
W--> 62 Xaa Xaa Leu Tyr Gly Gly Phe Arg Leu
E--> 63 1              5
    66 <210> SEQ ID NO: 3
    68 <211> LENGTH: 8
    70 <212> TYPE: PRT
    72 <213> ORGANISM: Artificial Sequence
    74 <220> FEATURE:
```

Does Not Comply
Corrected Diskette Needed

9 shown — needs explanation
9 (p.3) — needs explanation

needs explanation in ∠2207-∠2237 section / see item 11 on Err Summary Sheet)

see item 2 on Err Summary Sheet

```
76 <221> NAME/KEY: MISC_FEATURE
78 <222> LOCATION: (1)...(2)
```

RAW SEQUENCE LISTING   DATE: 03/14/2006
PATENT APPLICATION: US/09/926,493   TIME: 10:53:43

        Input Set : A:\PTO.DA.txt
        Output Set: N:\CRF4\03142006\I926493.raw

    80 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of the
antibody   *see item 2 on Exam*
    82 <400> SEQUENCE: 3   *Summary*
W--> 84 Xaa Xaa Tyr Leu Gly Gly Phe Arg Leu   *Sheet*
E--> 85 1   5
    88 <210> SEQ ID NO: 4
    90 <211> LENGTH: (8) 9
    92 <212> TYPE: PRT   *needs explanation*
    94 <213> ORGANISM: (Artificial Sequence)
    96 <220> FEATURE:
    98 <221> NAME/KEY: MISC_FEATURE
   100 <222> LOCATION: (1)...(2)
   102 <223> OTHER INFORMATION: Amino acids which allow chemical bonding or attachment of
the antibody   *see item 2 on Exam*
   104 <400> SEQUENCE: 4   *Summary*
W--> 106 Xaa Xaa Phe Phe Gly Gly Phe Arg Leu   *Sheet*
E--> 107 1   5

<210> 5   *last sequence in submitted file*

<211> 39

<212> PRT

<213> Haemophilus influenzae

<220>

<223> Biotinylated hemagglutinin fusogenic peptide

<400> 5

```
Gly Leu Phe Glu Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly
1               5                   10                  15
Met Ile Asp Gly Gly Gly Cys Gly Ser Gly Ser Tyr Thr Asp Ile Glu
            20                  25                  30
Met Asn Arg Leu Gly Lys Gly
            35
```

5

```
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:41 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:1
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:63 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:2
L:84 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:85 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:3
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:107 M:252 E: No. of Seq. differs, <211> LENGTH:Input:8 Found:9 SEQ:4
L:18 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (2) Counted (5)
```